In the claims:

Please amend the claims as follows:

1. (presently amended) A method of analyzing a plurality of target nucleic acid sequences in a sample, the method comprising:

providing, for each target nucleic acid sequence to be analyzed, at least one probe/primer molecule which ~~probe/primer molecule~~ includes a region of sequence substantially complementary to a sequence in the target nucleic acid sequence and ~~a region that is not located at either terminus of the probe/primer molecule and which includes~~ a capture tag sequence internal to a nucleic acid strand of said probe/primer molecule;

forming a reaction mixture which includes the probe/primer molecules and the target sequences under conditions such that, if a probe/primer molecule specific for a target sequence and that target sequence are both present, one or a plurality of derivative molecules having ~~a~~ said capture tag at one or both ~~its 3' or 5'~~ termini of a strand derived from~~, of~~ the probe/primer molecule specific for the target sequence, is generated; and

evaluating the presence of one or more derivative molecules, each derivative molecule indicating a target nucleic acid sequence in the sample, thereby analyzing the plurality of target nucleic acid sequences in the sample.

2. (original) The method of claim 1, wherein the derivative nucleic acid molecules are analyzed by hybridizing the tag sequences to capture probes which are spatially separated.

3. (original) The method of claim 2, wherein the capture probes are partially duplex probes with capture tag-complementary single stranded overhangs.

4. (original) The method of claim 2, wherein the capture tags are disposed on beads.

5. (original) The method of claim 2, wherein the capture tags are disposed on an ordered array.

6. (original) The method of claim 2, wherein the derivative nucleic acid is ligated to a capture probe and then washed.

Claims 7 – 35 (withdrawn)

36. (previously added) The method of claim 1, wherein the probe/primer molecule comprises a restriction endonuclease recognition site.

37. (previously added) The method of claim 36, wherein cleavage of the probe/primer molecule with the restriction endonuclease leaves the capture tag sequence in a single-stranded overhang.

38. (previously added) The method of claim 36, wherein the restriction endonuclease recognition site is a Type IIS restriction endonuclease recognition site.

39. (previously added) The method of claim 1, wherein the forming comprises cleaving probe/primer molecules that are annealed to target sequences with a restriction endonuclease.

40. (previously added) The method of claim 39, wherein the restriction endonuclease is a Type IIS restriction endonuclease.

41. (previously added) The method of claim 1, wherein the forming comprises cleaving probe/primer molecules with a flap endonuclease.

42. (previously added) A method of analyzing a sample of nucleic acids, the method comprising:

providing a plurality of probe molecules wherein the plurality comprises at least one probe molecule for each target nucleic acid sequence to be analyzed, the probe molecule comprising a region of sequence substantially complementary to a sequence in the target nucleic acid sequence and an internal capture tag sequence;

contacting the plurality of probe molecules to a sample of nucleic acids under conditions that allow a set of probe molecules for which a complementary sequence is present among the nucleic acids of the sample, to hybridize to the respective complementary sequence;

cleaving the probes molecules of the set, wherein the cleavage is specific for the probe molecules that hybridize to nucleic acids of the sample and the cleavage positions the capture tag sequence of each cleaved probe molecule at a terminus of the cleaved probe molecule; and

detecting one or more of the cleaved probes, thereby analyzing the sample of nucleic acids.

43. (previously added) The method of claim 42 wherein each probe molecule comprises a Type IIS restriction endonuclease recognition site positioned such that cleavage of the recognition site in a double stranded DNA into which the probe molecule is incorporated generates a nucleic acid having a single-stranded overhang that includes the tag sequence.

44. (new) The method of claim 42 wherein the cleaving positions the capture tag sequence of each cleaved probe molecule in a single-stranded overhang.

45. (new) The method of claim 44 wherein detecting comprises hybridizing capture tag sequences of the one or more cleaved probes to a plurality of capture probes.

46. (new) The method of claim 45 wherein each capture probe of the plurality of capture probes is immobilized.

47. (new) The method of claim 45 wherein each capture probe of the plurality of capture probes comprises a double stranded region and a single stranded region.

48. (new) The method of claim 47 wherein the 3' end of the single stranded region is extendable.

49. (new) The method of claim 47 wherein each capture probe of the plurality of capture probes forms a hairpin structure.

50. (new) The method of claim 47 wherein each capture probe of the plurality of capture probes comprises a chemical moiety that allows for immobilization.

51. (new) The method of claim 42 wherein detecting comprises hybridizing capture tag sequences of the one or more cleaved probes to a plurality of capture probes.

52. (new) The method of claim 51 wherein the detecting comprises an enzyme mediated reaction.

53. (new) The method of claim 52 wherein a derivative nucleic acid is a substrate or template for the enzyme mediated reaction.

54. (new) The method of claim 52 wherein a capture probe is a substrate or template for the enzyme mediated reaction.

55. (new) The method of claim 42 wherein the internal capture tag sequence of each probe molecule of the plurality of probe molecules is between 4 and 20 nucleotides in length.

56. (new) The method of claim 42 wherein the internal capture tag sequence of each probe molecule of the plurality of probe molecules is between 4 and 8 nucleotides in length.

57. (new) The method of claim 42 wherein the internal capture tag sequence of each probe molecule of the plurality of probe molecules is unique.

58. (new) The method of claim 46 further comprising ligating capture tag sequences of the one or more cleaved probes to capture probes of the plurality of capture probes.